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U.S. APPLICATION NUMBER NO.	FIRST NAMED APPLICANT	ATTY. DOCKET NO.
10/577,893	Steven W. Ludmerer	21564Y P
INTERNATIONAL APPLICATION NO.		
PCT/US04/36575		
210 MERCK AND CO., INC P O BOX 2000 RAHWAY, NJ 07065-0907	I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450, on the date appearing below. By <u>Shelley Kier</u> Date <u>1-24-07</u>	I.A. FILING DATE PRIORITY DATE 11/03/2004 11/05/2003
CONFIRMATION NO. 9691 371 FORMALITIES LETTER		
 *OC000900021849232*		

Date Mailed: 01/05/2007

NOTIFICATION TO COMPLY WITH REQUIREMENTS FOR PATENT APPLICATIONS CONTAINING NUCLEOTIDE AND/OR AMINO ACID SEQUENCE DISCLOSURES

Applicant is given **TWO MONTHS FROM THE DATE OF THIS NOTICE** within which to file the items indicated below to avoid abandonment. Extensions of time may be obtained under the provisions of 37 CFR 1.136(a).

- A copy of the "Sequence Listing" in computer readable form has been submitted. However, the content of the computer readable form does not comply with the requirements of 37 CFR 1.822 and/or 1.823, as indicated on the attached copy of the marked -up "Raw Sequence Listing." Applicant must provide a substitute computer readable form (CRF) copy of the "Sequence Listing" and a statement that the content of the sequence listing information recorded in computer readable form is identical to the written (on paper or compact disc) sequence listing and, where applicable, includes no new matter, as required by 37 CFR 1.821(e), 1.821(f), 1.821(g), 1.825(b), or 1.825(d).

Applicant is cautioned that correction of the above items may cause the specification and drawings page count to exceed 100 pages. If the specification and drawings exceed 100 pages, applicant will need to submit the required application size fee.

For questions regarding compliance to 37 CFR 1.821-1.825 requirements, please contact:

- **For Rules Interpretation, call (571) 272-0951**
- **For Patentin Software Program Help, call Patent EBC at 1-866-217-9197 or directly at 703-305-3028 / 703-308-6845 between the hours of 6 a.m. and 12 midnight, Monday through Friday, EST.**
- **Send e-mail correspondence for Patentin Software Program Help @ ebc@uspto.gov**

Applicant is reminded that any communications to the United States Patent and Trademark Office must be mailed to the address given in the heading and include the U.S. application no. shown above (37 CFR 1.5)

Registered users of EFS-Web may alternatively submit their reply to this notice via EFS-Web.
<https://sportal.uspto.gov/authenticate/AuthenticateUserLocalEPF.html>

For more information about EFS-Web please call the USPTO Electronic Business Center at 1-866-217-9197 or visit our website at <http://www.uspto.gov/ebc>.

If you are not using EFS-Web to submit your reply, you must include a copy of this notice.

DEBORAH D WILLIAMS

Telephone: (703) 308-9140 EXT 205

PART 1 - ATTORNEY/APPLICANT COPY

U.S. APPLICATION NUMBER NO.	INTERNATIONAL APPLICATION NO.	ATTY. DOCKET NO.
10/577,893	PCT/US04/36575	21564Y

FORM PCT/DO/EO/922 (371 Formalities Notice)

STIC Biotechnology Systems Branch

RAW SEQUENCE LISTING ERROR REPORT

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 10/577,893
Source: TPW/P
Date Processed by STIC: 05/11/2006

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) **INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) **TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION AND PATENTIN SOFTWARE QUESTIONS, PLEASE CONTACT MARK SPENCER, TELEPHONE: 571-272-2510; FAX: 571-273-0221

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 4.4.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW FOR ADDRESS:

<http://www.uspto.gov/web/offices/pac/checker/chkrnote.htm>

Applicants submitting genetic sequence information electronically on diskette or CD-Rom should be aware that there is a possibility that the disk/CD-Rom may have been affected by treatment given to all incoming mail.

Please consider using alternate methods of submission for the disk/CD-Rom or replacement disk/CD-Rom.

Any reply including a sequence listing in electronic form should NOT be sent to the 20231 zip code address for the United States Patent and Trademark Office, and instead should be sent via the following to the indicated addresses:

1. EFS-Bio (<http://www.uspto.gov/ebc/efs/downloads/documents.htm>), EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: Commissioner for Patents, P.O. Box 1450, Alexandria, VA 22313-1450
3. Hand Carry, Federal Express, United Parcel Service, or other delivery service (EFFECTIVE 01/14/05): U.S. Patent and Trademark Office, Mail Stop Sequence, Customer Window, Randolph Building, 401 Dulany Street, Alexandria, VA 22314

Revised 01/10/06

I hereby certify that this correspondence is being deposited with the United States Postal Service as first class mail in an envelope addressed to: Commissioner for Patents, P.O. Box 1450, Alexandria, Virginia 22313-1450, on the date appearing below.

MERCK & CO., INC.

By Susan Alex Date 1-24-07

BEST AVAILABLE COPY



IFWP

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/577,893

DATE: 05/11/2006
TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

4 <110> APPLICANT: Merck & Co., Inc.
 5 Istituto di Ricerche di Biologia Molecolare P. Angeletti S.p.A.
 7 <120> TITLE OF INVENTION: HCV REPLICONS CONTAINING NS5B FROM
 8 GENOTYPE 2B
 10 <130> FILE REFERENCE: 21564Y PCT
 C--> 12 <140> CURRENT APPLICATION NUMBER: US/10/577,893
 C--> 12 <141> CURRENT FILING DATE: 2006-05-01
 12 <150> PRIOR APPLICATION NUMBER: 60/517,605
 13 <151> PRIOR FILING DATE: 2003-11-05
 15 <160> NUMBER OF SEQ ID NOS: 28
 17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 591
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Artificial Sequence
 24 <220> FEATURE:
 25 <223> OTHER INFORMATION: modified NS5B
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 28 <222> LOCATION: (5)...(5)
 29 <223> OTHER INFORMATION: Xaa = threonine or serine
 W--> 31 <221> VARIANT
 32 <222> LOCATION: (24)...(24)
 33 <223> OTHER INFORMATION: Xaa = asparagine or serine
 W--> 35 <221> VARIANT
 36 <222> LOCATION: (31)...(31)
 37 <223> OTHER INFORMATION: Xaa = methionine or isoleucine
 W--> 39 <221> VARIANT
 40 <222> LOCATION: (376)...(376) → at this location 'Se'
 41 <223> OTHER INFORMATION: Xaa = isoleucine or leucine → at this location
 W--> 43 <400> 1
 W--> 44 Ser Met Ser Tyr Xaa Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro
 45 1 5 10 15
 W--> 46 Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg
 47 20 25 30
 48 Phe His Asn Lys Val Tyr Ser Thr Ser Arg Ser Ala Ser Leu Arg
 49 35 40 45
 50 Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr
 51 50 55 60
 52 Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala
 53 65 70 75 80
 54 Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser
 55 85 90 95
 56 Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser

Does Not Comply
Corrected Diskette Needed
(pg 1,2,6,7)

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/577,893.

DATE: 05/11/2006
TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

57	100	105	110
58	Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu		
59	115	120	125
60	Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val		
61	130	135	140
62	Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Pro Ala Arg Leu Ile		
63	145	150	155
64	Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr		
65	165	170	175
66	Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly		
67	180	185	190
68	Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp		
69	195	200	205
70	Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe		
71	210	215	220
72	Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr		
73	225	230	235
74	Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu		
75	245	250	255
76	Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln		
77	260	265	270
78	Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser		
79	275	280	285
80	Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys		
81	290	295	300
82	Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu		
83	305	310	315
84	Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu		
85	325	330	335
86	Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp		
87	340	345	350
88	Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser		
89	355	360	365
90	Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Tyr Phe Leu		
91	370	375	380
W-->	92 Thr Arg Asp Pro Thr Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val		
93	385	390	395
94	Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala		
95	405	410	415
96	Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile		
97	420	425	430
98	Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr		
99	435	440	445
100	Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu		
101	450	455	460
102	Arg Leu His Gly Leu Ala Phe Ser Leu His Thr Tyr Ser Pro His		
103	465	470	475
104	Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro		
105	485	490	495

? X98

RAW SEQUENCE LISTING DATE: 05/11/2006
 PATENT APPLICATION: US/10/577,893 TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT
 Output Set: N:\CRF4\05112006\J577893.raw

106 Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile
 107 500 505 510
 108 Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp
 109 515 520 525
 110 Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg
 111 530 535 540
 112 Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Asp Ile
 113 545 550 555 560
 114 Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Cys Leu
 115 565 570 575
 116 Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg
 117 580 585 590
 120 <210> SEQ ID NO: 2
 121 <211> LENGTH: 1776
 122 <212> TYPE: DNA
 123 <213> ORGANISM: Artificial Sequence
 125 <220> FEATURE:
 126 <223> OTHER INFORMATION: modified NS5B
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 129 <222> LOCATION: (3)...(3)
 130 <223> OTHER INFORMATION: n = A or T
 W--> 132 <221> variation
 133 <222> LOCATION: (9)...(9)
 134 <223> OTHER INFORMATION: n = C or A
 W--> 136 <221> variation
 137 <222> LOCATION: (13)...(13)
 138 <223> OTHER INFORMATION: n = A or T
 W--> 140 <221> variation
 141 <222> LOCATION: (15)...(15)
 142 <223> OTHER INFORMATION: n = A or C
 W--> 144 <221> variation
 145 <222> LOCATION: (21)...(21)
 146 <223> OTHER INFORMATION: n = A or G
 W--> 148 <221> variation
 149 <222> LOCATION: (24)...(24)
 150 <223> OTHER INFORMATION: n = C or G
 W--> 152 <221> variation
 153 <222> LOCATION: (28)...(28)
 154 <223> OTHER INFORMATION: n = T or C
 W--> 156 <221> modified_base
 157 <222> LOCATION: (30)...(30)
 158 <223> OTHER INFORMATION: n = G or C
 W--> 160 <221> variation
 161 <222> LOCATION: (33)...(33)
 162 <223> OTHER INFORMATION: n = C or A
 W--> 164 <221> variation
 165 <222> LOCATION: (71)...(71)
 166 <223> OTHER INFORMATION: n = A or G
 W--> 168 <221> variation

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/577,893

DATE: 05/11/2006

TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT
 Output Set: N:\CRF4\05112006\J577893.raw

```

169 <222> LOCATION: (83)...(83)
170 <223> OTHER INFORMATION: n = G or T
W--> 172 <221> variation
173 <222> LOCATION: (1174)...(1174)
174 <223> OTHER INFORMATION: n = A or C
W--> 176 <400> 2
W--> 177 tcnatgtcnt acncntggac nggngccntn atnacaccat gtggggccga agaggagaag 60
W--> 178 ttacccatca nccctcttag taattcgctc atncgggtcc ataataaggt gtactccaca 120
179 acctcgagga gtgcctctct gaggggcaaag aagggtactt ttgacagggt gcaggtgctg 180
180 gacgcacact atgactcagt cttgcaggac gtaagcggg ccgcctctaa ggtagtgcg 240
181 aggttcctca cggtagagga agcctgcgcg ctgacccccc cccactccgc caaatcgcga 300
182 tacggattt gggcaaaaaga ggtgcgcagc ttatcttagga gggccgttaa ccacatccgg 360
183 tccgtgtggg aggacctctt ggaagaccaa cataccccaa ttgacacaac tatcatggct 420
184 aaaaatgagg tgacctcat tcatccaact aaaggtggga aaaagccagc tcgcctcatc 480
185 .gtataaccccg.acctgggt.cagggtgtgc gaaaagatgg. ccctctatga..catcgacaaa 540.
186 aagttccca aagcgataat ggggccatcc tatgggttcc aatactctcc cgcagaacgg 600
187 gtcgatttcc tcctcaaagc ttggggaaat aagaaggacc caatgggtt ctcgtatgac 660
188 acccgctgtct ttgactcaac cgtcacggag agggacataa gaacagaaga atccatatat 720
189 caggcttgtt ctctgcctca agaagccaga actgtcatac actcgctcac tgagagactt 780
190 .tacgttaggag.ggccatgac.aaacagcaa gggcaatcct..gcggctacag..gcgttccgc. 840.
191 gcaageggtg ttttaccac cagcatggg aataccatga catgttacat caaagccctt 900
192 gcagcggtta aggctgcagg gatcggtggc cctgttatgt tgggtgtgtgg agacgacctg 960
193 gtcgtcatct cagagagcca aggttaacgag gaggacgagc gaaacacctgag agcttcacg 1020
194 gaggctatga ccaggtattc cggccctccc ggtgaccttc ccagacccggaa atatgacttg 1080
195 gagcttataa catctgcctc ctcaaactcta tcggtagcgc tggactctcg gggtcggccgc 1140
W--> 196 cggtaacttcc taaccagaga ccctaccact ccantcaccc gagctgtttt ggaaacagta 1200
197 agacactccc ctgtcaattt ttggctggc aacatcatcc agtacgcccc cacaatctgg 1260
198 gtccggatgg tcataatgac tcacttcttc tccatactat tggcccaagga cactctgaac 1320
199 caaaatctca atttgagat gtacggggca gtatactcgg tcaatccatt agaccttaccg 1380
200 gccataattt aaaggttaca ttggcttgaa gcctttcac tgcacacata ctctccccc 1440
201 gaactctcac ggggtggcagc aactctcaga aaacttggag cgcctccccc tagacgtgg 1500
202 aagagtcggg cgcgtgccgt gagagcttca ctcatcgcccc aaggagcggag ggcggccatt 1560
203 tgtggccgct accttctaa ctggggcggtt aaaacaaagc tcaaactcac tccattgccc 1620
204 gagggcgagcc gcctggattt atccgggtgg ttcaccgtgg ggcggccggg gggcgacatt 1680
205 tatcacagcg tgcgtcatgc ccgacccccc ctattactcc tttgtctact cctactttagc 1740
206 gtaggagtag gcatctttt actccccat cgatga 1776
208 <210> SEQ ID NO: 3
209 <211> LENGTH: 1394
210 <212> TYPE: PRT
211 <213> ORGANISM: Artificial Sequence
213 <220> FEATURE:
214 <223> OTHER INFORMATION: modified NS3-5A
W--> 216 <221> NAME/KEY: VARIANT
217 <222> LOCATION: (1215)...(1215)
218 <223> OTHER INFORMATION: Xaa = asparagine or serine
W--> 220 <221> VARIANT
221 <222> LOCATION: (904)...(904)
222 <223> OTHER INFORMATION: Xaa = valine or alanine
W--> 224 <400> 3

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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/577,893

DATE: 05/11/2006
TIME: 11:07:16

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

225 Met Ala Pro Ile Thr Ala Tyr Ser Gln Gln Thr Arg Gly Leu Leu Gly
 226 1 5 10 15
 227 Cys Ile Ile Thr Ser Leu Thr Gly Arg Asp Lys Asn Gln Val Glu Gly
 228 20 25 30
 229 Glu Val Gln Val Val Ser Thr Ala Thr Gln Ser Phe Leu Ala Thr Cys
 230 35 40 45
 231 Val Asn Gly Val Cys Trp Thr Val Tyr His Gly Ala Gly Ser Lys Thr
 232 50 55 60
 233 Leu Ala Gly Pro Lys Gly Pro Ile Thr Gln Met Tyr Thr Asn Val Asp
 234 65 70 75 80
 235 Gln Asp Leu Val Gly Trp Gln Ala Pro Pro Gly Ala Arg Ser Leu Thr
 236 85 90 95
 237 Pro Cys Thr Cys Gly Ser Ser Asp Leu Tyr Leu Val Thr Arg His Ala
 238 100 105 110
 239 Asp Val Ile Pro Val Arg Arg Gly Asp Ser Arg Gly Ser Leu Leu
 240 115 120 125
 241 Ser Pro Arg Pro Val Ser Tyr Leu Lys Gly Ser Ser Gly Gly Pro Leu
 242 130 135 140
 243 Leu Cys Pro Ser Gly His Ala Val Gly Ile Phe Arg Ala Ala Val Cys
 244 145 150 155 160
 245 Thr Arg Gly Val Ala Lys Ala Val Asp Phe Val Pro Val Glu Ser Met
 246 165 170 175
 247 Glu Thr Thr Met Arg Ser Pro Val Phe Thr Asp Asn Ser Ser Pro Pro
 248 180 185 190
 249 Ala Val Pro Gln Thr Phe Gln Val Ala His Leu His Ala Pro Thr Gly
 250 195 200 205
 251 Ser Gly Lys Ser Thr Lys Val Pro Ala Ala Tyr Ala Ala Gln Gly Tyr
 252 210 215 220
 253 Lys Val Leu Val Leu Asn Pro Ser Val Ala Ala Thr Leu Gly Phe Gly
 254 225 230 235 240
 255 Ala Tyr Met Ser Lys Ala His Gly Ile Asp Pro Asn Ile Arg Thr Gly
 256 245 250 255
 257 Val Arg Thr Ile Thr Thr Gly Ala Pro Val Thr Tyr Ser Thr Tyr Gly
 258 260 265 270
 259 Lys Phe Leu Ala Asp Gly Gly Cys Ser Gly Gly Ala Tyr Asp Ile Ile
 260 275 280 285
 261 Ile Cys Asp Glu Cys His Ser Thr Asp Ser Thr Thr Ile Leu Gly Ile
 262 290 295 300
 263 Gly Thr Val Leu Asp Gln Ala Glu Thr Ala Gly Ala Arg Leu Val Val
 264 305 310 315 320
 265 Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
 266 325 330 335
 267 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
 268 340 345 350
 269 Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe
 270 355 360 365
 271 Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
 272 370 375 380
 273 Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val

10/577,893

6

<210> 24

<211> 19

<212> DNA

<213> Artificial Sequence

<400> 24

gtctaccgtg agcgaggaa

If <213> Responses are
Artificial or Unknown.

Pls Explain the Source
of genetic Material.
See Item 11 on Error
Summary Sheet.

10/577,893

7

<210> 27

<211> 783

<212> DNA

<213> modified NS4B

<400> 27

22137 Responses can only
be Artificial, Unknown
or Genus Species. See
Item 10 on Error Summary
Sheet.

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/11/2006
PATENT APPLICATION: US/10/577,893 TIME: 11:07:17

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:1; Xaa Pos. 5,24,31,392
Seq#:2; N Pos. 3,9,13,15,21,24,28,30,33,71,93,1174
Seq#:3; Xaa Pos. 904,1215
Seq#:4; N Pos. 3644

Use of <220> Feature (NEW RULES):

Sequence(s) are missing the <220> Feature and associated headings.
Use of <220> to <223> is MANDATORY if <213> ORGANISM is "Artificial Sequence"
or "Unknown". Please explain source of genetic material in <220> to <223>
section (See "Federal Register," 6/01/98, Vol. 63, No. 104, pp. 29631-32)
(Sec.1.823 of new Rules)

Seq#:1,2,3,4,24

VERIFICATION SUMMARY

DATE: 05/11/2006

PATENT APPLICATION: US/10/577,893

TIME: 11:07:17

Input Set : A:\21564Y SEQ 05 01 06.TXT
Output Set: N:\CRF4\05112006\J577893.raw

L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:27 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:31 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:35 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:39 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:43 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:1
L:44 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:0
L:46 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:16
L:92 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1 after pos.:384
L:128 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:132 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:136 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:140 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:144 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:148 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:152 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
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L:164 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:168 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:172 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:176 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:2
L:177 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:60
L:196 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:2 after pos.:1140
L:216 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:220 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:224 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:3
L:337 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:896
L:375 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:1200
L:411 M:281 W: Numeric Fields not Ordered, <221> Sort in ascending order!
L:415 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:419 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ ID#:4
L:480 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4 after pos.:3600
L:703 M:220 C: Keyword misspelled or invalid format, <213> ORGANISM for SEQ ID#:24
L:705 M:258 W: Mandatory Feature missing, <220> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Tag not found for SEQ#:24, <213>
ORGANISM:Artificial Sequence
L:705 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:24, Line#:705

21564YP

SEQUENCE LISTING

<110> Ludmerer, Steven W.
Graham, Donald J.
LaFemina, Robert L.
Flores, Osvaldo A.
Pizzuti, Maura
Traboni, Cinzia

<120> HCV REPLICONS CONTAINING NS5B FROM
GENOTYPE 2B

<130> 21564YP

<140> 10/577,893
<141> 2006-05-01

<150> PCT/US2004/036575
<151> 2004-11-03

<150> 60/517,605
<151> 2003-11-05

<160> 28

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 591
<212> PRT
<213> Artificial Sequence

<220>
<223> modified NS5B

<221> VARIANT
<222> (5)...(5)
<223> Xaa = threonine or serine

<221> VARIANT
<222> (24)...(24)
<223> Xaa = asparagine or serine

<221> VARIANT
<222> (31)...(31)
<223> Xaa = methionine or isoleucine

<221> VARIANT
<222> (392)...(392)
<223> Xaa = isoleucine or leucine

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1 5 10 15

Glu Glu Glu Lys Leu Pro Ile Xaa Pro Leu Ser Asn Ser Leu Xaa Arg
 20 25 30
 Phe His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg
 35 40 45
 Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His Tyr
 50 55 60
 Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val Ser Ala
 65 70 75 80
 Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro Pro His Ser
 85 90 95
 Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val Arg Ser Leu Ser
 100 105 110
 Arg Arg Ala Val Asn His Ile Arg Ser Val Trp Glu Asp Leu Leu Glu
 115 120 125
 Asp Gln His Thr Pro Ile Asp Thr Thr Ile Met Ala Lys Asn Glu Val
 130 135 140
 Phe Cys Ile Asp Pro Thr Lys Gly Gly Lys Lys Pro Ala Arg Leu Ile
 145 150 155 160
 Val Tyr Pro Asp Leu Gly Val Arg Val Cys Glu Lys Met Ala Leu Tyr
 165 170 175
 Asp Ile Ala Gln Lys Leu Pro Lys Ala Ile Met Gly Pro Ser Tyr Gly
 180 185 190
 Phe Gln Tyr Ser Pro Ala Glu Arg Val Asp Phe Leu Leu Lys Ala Trp
 195 200 205
 Gly Ser Lys Lys Asp Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe
 210 215 220
 Asp Ser Thr Val Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr
 225 230 235 240
 Gln Ala Cys Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu
 245 250 255
 Thr Glu Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln
 260 265 270
 Ser Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser
 275 280 285
 Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys Lys
 290 295 300
 Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp Asp Leu
 305 310 315 320
 Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu Arg Asn Leu
 325 330 335
 Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala Pro Pro Gly Asp
 340 345 350
 Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile Thr Ser Cys Ser Ser
 355 360 365
 Asn Val Ser Val Ala Leu Asp Ser Arg Gly Arg Arg Arg Tyr Phe Leu
 370 375 380
 Thr Arg Asp Pro Thr Pro Xaa Thr Arg Ala Ala Trp Glu Thr Val
 385 390 395 400
 Arg His Ser Pro Val Asn Ser Trp Leu Gly Asn Ile Ile Gln Tyr Ala
 405 410 415
 Pro Thr Ile Trp Val Arg Met Val Ile Met Thr His Phe Phe Ser Ile
 420 425 430
 Leu Leu Ala Gln Asp Thr Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr
 435 440 445

Gly Ala Val Tyr Ser Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu
 450 455 460
 Arg Leu His Gly Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His
 465 470 475 480
 Glu Leu Ser Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro
 485 490 495
 Leu Arg Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile
 500 505 510
 Ala Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp
 515 520 525
 Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser Arg
 530 535 540
 Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Asp Ile
 545 550 555 560
 Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu Leu Cys Leu
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 Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu Pro Asp Arg
 580 585 590

<210> 2
 <211> 1776
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified NS5B

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 <223> n = A or T

<221> variation
 <222> (9)...(9)
 <223> n = C or A

<221> variation
 <222> (13)...(13)
 <223> n = A or T

<221> variation
 <222> (15)...(15)
 <223> n = A or C

<221> variation
 <222> (21)...(21)
 <223> n = A or G

<221> variation
 <222> (24)...(24)
 <223> n = C or G

<221> variation
 <222> (28)...(28)
 <223> n = T or C

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<221> modified_base
<222> (30)...(30)
<223> n = G or C

<221> variation
<222> (33)...(33)
<223> n = C or A

<221> variation
<222> (71)...(71)
<223> n = A or G

<221> variation
<222> (83)...(83)
<223> n = G or T

<221> variation
<222> (1174)...(1174)
<223> n = A or C

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gacgcacact atgactcagt cttgcagagc gttaagcggg ccgcctctaa ggtagtgcg 240
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gtataccccg accttggggt cagggtgtgc gaaaagatgg ccctctatga catcgacaaa 540
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gtcgatttcc tcctcaaagc ttggggaaagt aagaaggacc caatgggtt ctcgtatgac 660
acccgctgtt ttgactcaac cgtcacggag agggacataa gaacagaaga atccatatat 720
caggcttggt ctctgcctca agaagccaga actgtcatac actcgctcac tgagagactt 780
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gcaagcggtt ttttaccac cagcatgggg aataccatga catgttacat caaaggccct 900
gcagcgtgtt aggctgcagg gatcgtggac cctgttatgt tgggtgtgg agacgacctg 960
gtcgtcatct cagagagcca aggttaacggag gaggacgagc gaaacctgag agctttcacg 1020
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gagcttataa catcctgctc ctcaaacgta tcgttagcgc tggactctcg gggtcgcgc 1140
cggtacttcc taaccagaga ccctaccact ccantcaccc gagctgctt gggaaacagta 1200
agacactccc ctgtcaattt ttggctggc aacatcatcc agtaccccc cacaatctgg 1260
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caaatctca atttgagat gtacggggca gtatactcgg tcaatccatt agacctaccg 1380
gcataattt aaaggctaca tgggcttggaa gcctttcac tgcacacata ctctccccac 1440
gaactctcac gggtggcagc aactctcaga aaacttggag cgccctccct tagagcgtgg 1500
aagagtcggg cgcgtccgt gagagcttca ctcatcgccc aaggagcgg ggcggccatt 1560
tgtggccgtt acctttcaa ctggcggtt aaaacaaagc tcaaactcac tccattgc 1620
gaggcgagcc gcctggattt atccgggtt ttcaccgtgg ggcggccgg gggcgacatt 1680
tatcacagcg tgcgtcatgc ccgaccccgcc ctattactcc tttgcctact cctacttagc 1740
gtaggagtag gcatttttt actccccat cgatga 1776

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<210> 3
<211> 1394
<212> PRT

<213> Artificial Sequence

<220>

<223> modified NS3-5A

<221> VARIANT

<222> (1215)...(1215)

<223> Xaa = asparagine or serine

<221> VARIANT

<222> (904)...(904)

<223> Xaa = valine or alanine

<400> 3

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								20		25					30
Glu	Val	Gln	Val	Val	Ser	Thr	Ala	Thr	Gln	Ser	Phe	Leu	Ala	Thr	Cys
								35		40					45
Val	Asn	Gly	Val	Cys	Trp	Thr	Val	Tyr	His	Gly	Ala	Gly	Ser	Lys	Thr
								50		55					60
Leu	Ala	Gly	Pro	Lys	Gly	Pro	Ile	Thr	Gln	Met	Tyr	Thr	Asn	Val	Asp
								65		70		75			80
Gln	Asp	Leu	Val	Gly	Trp	Gln	Ala	Pro	Pro	Gly	Ala	Arg	Ser	Leu	Thr
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Pro	Cys	Thr	Cys	Gly	Ser	Ser	Asp	Leu	Tyr	Leu	Val	Thr	Arg	His	Ala
								100		105					110
Asp	Val	Ile	Pro	Val	Arg	Arg	Gly	Asp	Ser	Arg	Gly	Ser	Leu	Leu	
								115		120					125
Ser	Pro	Arg	Pro	Val	Ser	Tyr	Leu	Lys	Gly	Ser	Ser	Gly	Gly	Pro	Leu
								130		135					140
Leu	Cys	Pro	Ser	Gly	His	Ala	Val	Gly	Ile	Phe	Arg	Ala	Ala	Val	Cys
								145		150		155			160
Thr	Arg	Gly	Val	Ala	Lys	Ala	Val	Asp	Phe	Val	Pro	Val	Glu	Ser	Met
								165		170					175
Glu	Thr	Thr	Met	Arg	Ser	Pro	Val	Phe	Thr	Asp	Asn	Ser	Ser	Pro	Pro
								180		185					190
Ala	Val	Pro	Gln	Thr	Phe	Gln	Val	Ala	His	Leu	His	Ala	Pro	Thr	Gly
								195		200					205
Ser	Gly	Lys	Ser	Thr	Lys	Val	Pro	Ala	Ala	Tyr	Ala	Ala	Gln	Gly	Tyr
								210		215					220
Lys	Val	Leu	Val	Leu	Asn	Pro	Ser	Val	Ala	Ala	Thr	Leu	Gly	Phe	Gly
								225		230		235			240
Ala	Tyr	Met	Ser	Lys	Ala	His	Gly	Ile	Asp	Pro	Asn	Ile	Arg	Thr	Gly
								245		250					255
Val	Arg	Thr	Ile	Thr	Thr	Gly	Ala	Pro	Val	Thr	Tyr	Ser	Thr	Tyr	Gly
								260		265					270
Lys	Phe	Leu	Ala	Asp	Gly	Gly	Cys	Ser	Gly	Gly	Ala	Tyr	Asp	Ile	Ile
								275		280					285
Ile	Cys	Asp	Glu	Cys	His	Ser	Thr	Asp	Ser	Thr	Thr	Ile	Leu	Gly	Ile
								290		295					300
Gly	Thr	Val	Leu	Asp	Gln	Ala	Glu	Thr	Ala	Gly	Ala	Arg	Leu	Val	Val
								305		310		315			320

Leu Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Val Pro His Pro Asn
 325 330 335
 Ile Glu Glu Val Ala Leu Ser Asn Thr Gly Glu Ile Pro Phe Tyr Gly
 340 345 350
 Lys Ala Ile Pro Ile Glu Ala Ile Arg Gly Gly Arg His Leu Ile Phe
 355 360 365
 Cys His Ser Lys Lys Cys Asp Glu Leu Ala Ala Lys Leu Ser Gly
 370 375 380
 Leu Gly Ile Asn Ala Val Ala Tyr Tyr Arg Gly Leu Asp Val Ser Val
 385 390 395 400
 Ile Pro Thr Ile Gly Asp Val Val Val Ala Thr Asp Ala Leu Met
 405 410 415
 Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val Ile Asp Cys Asn Thr Cys
 420 425 430
 Val Thr Gln Thr Val Asp Phe Ser Leu Asp Pro Thr Phe Thr Ile Glu
 435 440 445
 Thr Thr Thr Val Pro Gln Asp Ala Val Ser Arg Ser Gln Arg Arg Gly
 450 455 460
 Arg Thr Gly Arg Gly Arg Met Gly Ile Tyr Arg Phe Val Thr Pro Gly
 465 470 475 480
 Glu Arg Pro Ser Gly Met Phe Asp Ser Ser Val Leu Cys Glu Cys Tyr
 485 490 495
 Asp Ala Gly Cys Ala Trp Tyr Glu Leu Thr Pro Ala Glu Thr Ser Val
 500 505 510
 Arg Leu Arg Ala Tyr Leu Asn Thr Pro Gly Leu Pro Val Cys Gln Asp
 515 520 525
 His Leu Glu Phe Trp Glu Ser Val Phe Thr Gly Leu Thr His Ile Asp
 530 535 540
 Ala His Phe Leu Ser Gln Thr Lys Gln Ala Gly Asp Asn Phe Pro Tyr
 545 550 555 560
 Leu Val Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Gln Ala Pro Pro
 565 570 575
 Pro Ser Trp Asp Gln Met Trp Lys Cys Leu Ile Arg Leu Lys Pro Thr
 580 585 590
 Leu His Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val Gln Asn
 595 600 605
 Glu Val Thr Leu Thr His Pro Ile Thr Lys Tyr Ile Met Ala Cys Met
 610 615 620
 Ser Ala Asp Leu Glu Val Val Thr Ser Thr Trp Val Leu Val Gly Gly
 625 630 635 640
 Val Leu Ala Ala Leu Ala Ala Tyr Cys Leu Thr Thr Gly Ser Val Val
 645 650 655
 Ile Val Gly Arg Ile Ile Leu Ser Gly Arg Pro Ala Ile Val Pro Asp
 660 665 670
 Arg Glu Phe Leu Tyr Gln Glu Phe Asp Glu Met Glu Glu Cys Ala Ser
 675 680 685
 His Leu Pro Tyr Ile Glu Gln Gly Met Gln Leu Ala Glu Gln Phe Lys
 690 695 700
 Gln Lys Ala Leu Gly Leu Leu Gln Thr Ala Thr Lys Gln Ala Glu Ala
 705 710 715 720
 Ala Ala Pro Val Val Glu Ser Lys Trp Arg Ala Leu Glu Thr Phe Trp
 725 730 735
 Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly
 740 745 750

Leu Ser Thr Leu Pro Gly Asn Pro Ala Ile Ala Ser Leu Met Ala Phe
 755 760 765
 Thr Ala Ser Ile Thr Ser Pro Leu Thr Thr Gln Ser Thr Leu Leu Phe
 770 775 780
 Asn Ile Leu Gly Gly Trp Val Ala Ala Gln Leu Ala Pro Pro Ser Ala
 785 790 795 800
 Ala Ser Ala Phe Val Gly Ala Gly Ile Ala Gly Ala Ala Val Gly Ser
 805 810 815
 Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly Ala
 820 825 830
 Gly Val Ala Gly Ala Leu Val Ala Phe Lys Val Met Ser Gly Glu Met
 835 840 845
 Pro Ser Thr Glu Asp Leu Val Asn Leu Leu Pro Ala Ile Leu Ser Pro
 850 855 860
 Gly Ala Leu Val Val Gly Val Val Cys Ala Ala Ile Leu Arg Arg His
 865 870 875 880
 Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu Ile Ala
 885 890 895
 Phe Ala Ser Arg Gly Asn His Xaa Ser Pro Thr His Tyr Val Pro Glu
 900 905 910
 Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu Thr Ile
 915 920 925
 Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp Cys Ser
 930 935 940
 Thr Pro Cys Ser Gly Ser Trp Leu Arg Asp Val Trp Asp Trp Ile Cys
 945 950 955 960
 Thr Val Leu Thr Asp Phe Lys Thr Trp Leu Gln Ser Lys Leu Leu Pro
 965 970 975
 Gln Leu Pro Gly Val Pro Phe Phe Ser Cys Gln Arg Gly Tyr Lys Gly
 980 985 990
 Val Trp Arg Gly Asp Gly Ile Met Gln Thr Thr Cys Pro Cys Gly Ala
 995 1000 1005
 Gln Ile Thr Gly His Val Lys Asn Gly Ser Met Arg Ile Val Gly Pro
 1010 1015 1020
 Lys Thr Cys Ser Asn Thr Trp His Gly Thr Phe Pro Ile Asn Ala Tyr
 1025 1030 1035 1040
 Thr Thr Gly Pro Cys Thr Pro Ser Pro Ala Pro Asn Tyr Ser Arg Ala
 1045 1050 1055
 Leu Trp Arg Val Ala Ala Glu Glu Tyr Val Glu Val Thr Arg Val Gly
 1060 1065 1070
 Asp Phe His Tyr Val Thr Gly Met Thr Thr Asp Asn Val Lys Cys Pro
 1075 1080 1085
 Cys Gln Val Pro Ala Pro Glu Phe Phe Thr Glu Val Asp Gly Val Arg
 1090 1095 1100
 Leu His Arg Tyr Ala Pro Ala Cys Arg Pro Leu Leu Arg Glu Glu Val
 1105 1110 1115 1120
 Thr Phe Gln Val Gly Leu Asn Gln Tyr Leu Val Gly Ser Gln Leu Pro
 1125 1130 1135
 Cys Glu Pro Glu Pro Asp Val Ala Val Leu Thr Ser Met Leu Thr Asp
 1140 1145 1150
 Pro Ser His Ile Thr Ala Glu Thr Ala Lys Arg Arg Leu Ala Arg Gly
 1155 1160 1165
 Ser Pro Pro Ser Leu Ala Ser Ser Ser Ala Ile Gln Leu Ser Ala Pro
 1170 1175 1180

Ser Leu Lys Ala Thr Cys Thr Thr His His Val Ser Pro Asp Ala Asp
 1185 1190 1195 1200
 Leu Ile Glu Ala Asn Leu Leu Trp Arg Gln Glu Met Gly Gly Xaa Ile
 1205 1210 1215
 Thr Arg Val Glu Ser Glu Asn Lys Val Val Val Leu Asp Ser Phe Asp
 1220 1225 1230
 Pro Leu Arg Ala Glu Glu Asp Glu Arg Glu Val Ser Val Pro Ala Glu
 1235 1240 1245
 Ile Leu Arg Lys Ser Lys Lys Phe Pro Ala Ala Met Pro Ile Trp Ala
 1250 1255 1260
 Arg Pro Asp Tyr Asn Pro Pro Leu Leu Glu Ser Trp Lys Asp Pro Asp
 1265 1270 1275 1280
 Tyr Val Pro Pro Val Val His Gly Cys Pro Leu Pro Pro Ile Lys Ala
 1285 1290 1295
 Pro Pro Ile Pro Pro Arg Arg Lys Arg Thr Val Val Leu Thr Glu
 1300 1305 1310
 Ser Ser Val Ser Ser Ala Leu Ala Glu Leu Ala Thr Lys Thr Phe Gly
 1315 1320 1325
 Ser Ser Glu Ser Ser Ala Val Asp Ser Gly Thr Ala Thr Ala Leu Pro
 1330 1335 1340
 Asp Gln Ala Ser Asp Asp Gly Asp Lys Gly Ser Asp Val Glu Ser Tyr
 1345 1350 1355 1360
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<210> 4
 <211> 4182
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> modified NS3-5A

<221> variation
 <222> (2711)...(2711)
 <223> n = T or C

<221> variation
 <222> (3645)...(3645)
 <223> n = A or G

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35 40 45
Phe Trp Ala Lys His Met Trp Asn Phe Ile Ser Gly Ile Gln Tyr Leu
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Ala Gly Leu Ser Thr Leu Pro Gly Asn Pro Ala Val Ala Ser Met Met
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Ala Phe Ser Ala Ala Leu Thr Ser Pro Leu Pro Thr Ser Thr Thr Ile
85 90 95
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115 120 125
Gly Ser Ile Gly Leu Gly Lys Ile Leu Val Asp Val Leu Ala Gly Tyr
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Gly Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly
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Glu Lys Pro Thr Val Glu Asp Val Val Asn Leu Leu Pro Ala Ile Leu
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Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala Ile Leu Arg
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Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met Asn Arg Leu
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Ile Ala Phe Ala Ser Arg Gly Asn His Ala Ser Pro Thr His Tyr Val
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Pro Glu Ser Asp Ala Ala Ala Arg Val Thr Gln Ile Leu Ser Ser Leu
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Thr Ile Thr Gln Leu Leu Lys Arg Leu His Gln Trp Ile Asn Glu Asp
245 250 255
Cys Ser Thr Pro Cys
260